

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 14, 2001, 02:37:58 ; Search time 52.5 seconds

(without alignments)
434.564 Million cell updates/sec

Title: US-09-481-990-2

Perfect score: 1753

Sequence: 1 M0SLAGSSCVLRHRSRHA.....QNEPVTATQSSACVDPANH 336

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Archived: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR.66:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 1753 | 100.0 | 336 | 2 | S65566 inward rectifier p |
| 2 | 430.5 | 24.6 | 392 | 2 | T45032 hypothetical prote |
| 3 | 300 | 17.1 | 393 | 2 | T25392 hypothetical prote |
| 4 | 295 | 16.8 | 427 | 2 | T27681 hypothetical prote |
| 5 | 294.5 | 16.8 | 443 | 2 | T21598 hypothetical prote |
| 6 | 294 | 16.8 | 334 | 2 | T19860 hypothetical prote |
| 7 | 294 | 16.8 | 364 | 2 | T43361 probable potassium |
| 8 | 291 | 16.6 | 329 | 2 | T43509 outward rectifier |
| 9 | 284.5 | 16.2 | 336 | 2 | T32347 potassium channel |
| 10 | 264.5 | 15.1 | 1001 | 2 | T13807 hypothetical prote |
| 11 | 256.5 | 14.6 | 475 | 2 | T27725 hypothetical prote |
| 12 | 251 | 14.3 | 383 | 2 | T23182 hypothetical prote |
| 13 | 246 | 14.0 | 522 | 2 | T24265 hypothetical prote |
| 14 | 244 | 13.9 | 631 | 2 | T26232 hypothetical prote |
| 15 | 244 | 13.9 | 513 | 2 | T28933 hypothetical prote |
| 16 | 240 | 13.7 | 539 | 2 | T23700 hypothetical prote |
| 17 | 236 | 13.5 | 528 | 2 | T21834 hypothetical prote |
| 18 | 231 | 13.2 | 523 | 2 | T23373 hypothetical prote |
| 19 | 226.5 | 12.9 | 383 | 2 | T23746 hypothetical prote |
| 20 | 222.5 | 12.7 | 335 | 2 | S44635 hypothetical prote |
| 21 | 222 | 12.7 | 524 | 2 | T23907 f2227.7 protein - |
| 22 | 222 | 12.7 | 1539 | 2 | T30037 hypothetical prote |
| 23 | 219.5 | 12.5 | 700 | 2 | T27364 hypothetical prote |
| 24 | 213.5 | 12.2 | 485 | 2 | T24201 hypothetical prote |
| 25 | 211.5 | 12.1 | 769 | 2 | T27550 hypothetical prote |
| 26 | 209.5 | 12.0 | 660 | 2 | T21551 hypothetical prote |
| 27 | 209 | 11.9 | 452 | 2 | T21118 hypothetical prote |
| 28 | 204 | 11.6 | 544 | 2 | T43364 potassium channel |
| 29 | 204 | 11.6 | 576 | 2 | T43363 potassium channel |

| | | | | | |
|----|-------|------|------|---|---------------------------|
| 30 | 204 | 11.6 | 643 | 2 | T26616 hypothetical prote |
| 31 | 199.5 | 11.4 | 1136 | 2 | T26953 hypothetical prote |
| 32 | 199 | 11.4 | 681 | 2 | T19429 hypothetical prote |
| 33 | 194.5 | 11.1 | 405 | 2 | T21188 hypothetical prote |
| 34 | 192 | 11.0 | 600 | 2 | T43531 hypothetical prote |
| 35 | 192 | 11.0 | 600 | 2 | T24626 hypothetical prote |
| 36 | 190.5 | 10.9 | 325 | 2 | T15584 hypothetical prote |
| 37 | 190.5 | 10.9 | 484 | 2 | T43529 probable potassium |
| 38 | 190.5 | 10.9 | 519 | 2 | T16629 hypothetical prote |
| 39 | 190 | 10.8 | 504 | 2 | T22269 hypothetical prote |
| 40 | 189 | 10.8 | 550 | 2 | T22557 hypothetical prote |
| 41 | 188.5 | 10.8 | 551 | 2 | T16426 hypothetical prote |
| 42 | 188.5 | 10.8 | 555 | 2 | T43357 potassium channel |
| 43 | 187 | 10.7 | 381 | 2 | T43393 potassium channel |
| 44 | 183.5 | 10.5 | 586 | 2 | T21683 hypothetical prote |
| 45 | 180.5 | 10.3 | 461 | 2 | T43394 potassium channel |

ALIGNMENTS

```

RESULT
1
S65566
inward rectifier potassium channel TWIK-1 - human
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S65566
R:Lesage, F.; Guillemaire, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanl
EMBO J. 15, 1004-1011, 1996
A>Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a nove
A:Reference number: S65566; M01D:96183184
A:Accession: S65566
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <LES>
A:Cross-references: EMBL:U033632; NID:g1086490; P10N:AAB01688.1; PID:g1086491

Query Match      100.0%; Score 1753; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.5e-146;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 M0SLAGSSCVLRHRSRHA...QNEPVTATQSSACVDPANH 60
    |||||||
DB 1 M0SLAGSSCVLRHRSRHA...QNEPVTATQSSACVDPANH 60
    |||||||

QY 61 RRFLEHECLSEOOLEDFLGVLEASNYGVSLNASGNMMDFTSALFFASTVLTSTGY 120
    |||||||
DB 61 RRFLEHECLSEOOLEDFLGVLEASNYGVSLNASGNMMDFTSALFFASTVLTSTGY 120
    |||||||

QY 121 GHVPLSDGKAFCIIVSVIGIPFTLLFLNAVORITVHTRRPVLYPHIRMGFSKQYVA 180
    |||||||
DB 121 GHVPLSDGKAFCIIVSVIGIPFTLLFLNAVORITVHTRRPVLYPHIRMGFSKQYVA 180
    |||||||

QY 181 IVHAVILGFVTVSGFFPRPAVEVLEDDNMFSLSFYCFSLSTIGDGVVPGGYNOX 240
    |||||||
DB 181 IVHAVILGFVTVSGFFPRPAVEVLEDDNMFSLSFYCFSLSTIGDGVVPGGYNOX 240
    |||||||

QY 241 FRELXKIGITCYLLGLTAMLVLETFCELHELKKFRKMFYVKKDKDDQVHIIEHDLS 300
    |||||||
DB 241 FRELXKIGITCYLLGLTAMLVLETFCELHELKKFRKMFYVKKDKDDQVHIIEHDLS 300
    |||||||

QY 301 FSSITDQAAGKEDQKONEPVTATQSSACVDPANH 336
    |||||||
DB 301 FSSITDQAAGKEDQKONEPVTATQSSACVDPANH 336
    |||||||

RESULT
2
T45032
hypothetical protein Y39B6.f [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45032

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R:Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, Taser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns, B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D.; Nature 368, 32-38, 1994
 A:Authors: Shownkeen, R.; Sims, M.; Smaiden, N.; Smith, A.; Smith, M.; Sonhammer, E.; Slock, L.; Wilkinson-Sprat, J.; Whildman, P.
 A:Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
 A:Reference number: S43531; M01D:94150718
 A:Accession: T45032
 A:Status: preliminary; translated from GB/EMBL/DBD
 A:Molecule type: DNA
 A:Residues: 1-392 <WILL>
 A:Cross-references: EMBL:AL12896; NID:96434440; PIDN:CAB60911.1; PID:96434446
 A:Experimental source: clone Y39B6B
 C:Genetics:
 A:Map position: 3
 A:Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3
 A:Note: Y39B6B.f

Query Match

Best Local Similarity 24.6%; Score 430.5; DB 2; Length 392;
 Matches 101; Conservative 47; Mismatches 83; Indels 33; Gaps 7;

QY 41 FSSVELPYEDLROELRKRLRLE-HECLSEQLEQFLGRVLEASNYGVSLSNAG 98
 DB 118 FSRIFPEKIEFEAYLDIQOMWRDLIDLDSEIDKFLNIREAALNGIMDRNLT 177
 QY 99 NNMWDTSLFFASVLTSTGTVPLSDGKAFCTIYVIGIPTLLFLAVGQRTIV 158
 DB 178 DPMWFGQAFEGAGTLISVYGGRVSPREYGLFLILCVIGIPTLLSLVAKM-- 235
 QY 159 HTRRVYLFHIRMGSKQ-----VVAIVAVLLGFVYSCFFPIPAVFS 204
 DB 236 ---REP---SHLRGLNORLGHLEFTVNHILQIHGVGVFASILLFV----PAIPAWFS 284
 QY 205 VLEDWMNFESEFYCFISTIGLDGYVEGYNOKERELXKIGITCYLLGLIAMLVYL 264
 DB 285 SIETDMSYDARVYCVSLTITGLDGFEGDDPNOSFRLGKIGAVYLMGGLCCMMFL 344
 QY 265 EFCELHELEKFR-KMFYVKKDKD 287
 DB 345 AT---LYDIPQNLTSFFVKSDEE 365

RESULT 3

T25392

hypothetical protein T28A8.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

A:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 #accession: T25392

Kiloyd, C.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z20027

A:Accession: T25392

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-393 <WILL>

A:Cross-references: EMBL:Z2813; PIDN:CAB07286.1; GSPDB:GN00021; CESP:T28A8.1

A:Experimental source: clone T28A8

C:Genetics:

A:Gene: CESP:T28A8.1

A:Map position: 3

A:Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2

Query Match

Best Local Similarity 17.1%; Score 300; DB 2; Length 393;
 Matches 93; Conservative 72; Mismatches 110; Indels 88; Gaps 15;

QY 12 RLVHRHSACFCFLVGLVLYLVFGAVVSSVELPYEDLRO---ELRLKRLRLEEH- 67
 DB 9 RILAHVS-----LVLAVVYVGFAGFLFYOLEPQNEVEVRANIERFNIHRKROMIEHL 62

QY 68 -----ECLEEQLEQFLGRVLEASN---YGVSL--SNASGNMNDPISALF 109
 DB 63 WEMRESGIGHVEDLAVKVDVNTRLPEAFPTROIGAKHLRPGGDEDEYNTMTALF 122
 QY 110 FASVLTSTGTVPLSDGKAFCTIYVIGIPTLLFLAVGQRTIVHTRRVLYPH 169
 DB 123 FTTLLTITGYNMLTPVGRKLCILYALFVPLILITVADIGKLSNIYQLTWYRK 182
 QY 170 IRMGSKOVAIYH-----AVLLGFVSCFFPIPA 201
 DB 183 LRKCKOKKQKSVLSSDDKNEGLMDHLENTISIPFLVAILLSYITFG-----AV 236
 QY 202 VPSVLEDWMNFESEFYCFISTIGLDGYVEGYNOKERELXKIGITCYLLGLIAML 261
 DB 237 VLSMWE-GMDFESGFYSFTMTVGFQDIPLK-----REYILDL-CYIIIGL---- 284
 QY 262 VLEDFEC-ELHELEKFRKMFY-KDKDE-----DQVHIEHDLSFSSITDQAG 310
 DB 285 -STTYMCIDLVGIOYIRKMHYGRALKARFALVNVGKRMHV--PDLMRYASVLDQKYG 341
 QY 311 MKE 313
 DB 342 QKK 344

RESULT 4

T27681

hypothetical protein ZK1067.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

A:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 #accession: T27681

R.Thomas, K.

submitted to the EMBL Data Library, March 1996

A:Reference number: Z20404

A:Accession: T27681

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-427 <WILL>

A:Cross-references: EMBL:Z70038; PIDN:CAA93881.1; GSPDB:GN00020; CESP:ZK1067.5

A:Experimental source: clone ZK1067

C:Genetics:

A:Gene: CESP:ZK1067.5

A:Map position: 2

A:Introns: 51/3; 123/1; 212/1; 261/2; 331/3; 365/1; 394/2; 414/3

Query Match

Best Local Similarity 16.8%; Score 295; DB 2; Length 427;
 Matches 82; Conservative 51; Mismatches 82; Indels 94; Gaps 10;

QY 26 LVLYGLVLYLVFGAVVSSVELPYEDLROELRKRLRLEEHCLSEQLEQFLGRVLEA 85
 DB 137 LIPATVAYITAGALFKEIEHQALDRYQSYHTYR-----NFNINLYQS 181
 QY 86 SNYGVSVLSN-----ASGNW-----NMDFSLAFASVLTSTG 121
 DB 182 SNRSVADVENVLIDPFSINRAKREGIKPTDLPQETSMSISALFFTYLVLSIGV 241
 QY 122 HYPVLSGKAFCTIYVIGIPTLLFLT---AVQRTVHTRRVLYPHIRMGSKQ 177
 DB 242 NLPISITSGKIFCVGAIRGIPLTIVTIADLAKFVADMIMPTEDPKT-----GRQ 293
 QY 178 VVAIVHAVLLGFVYSCFFPIPAVSVLEDMNFESEFYCFISTIGLDGYVPBG 237
 DB 294 LVLV--FLIGYMTIS-----ACVTTILEPMSFSDSFCLVSLITVGFCD----- 338
 QY 238 NOKFRELYVIGITCYLL-----LGLIAMLVLEET-----FCELHELEK 275
 DB 339 -----LHVGVTEVYMLCSIVFIFGLITLITLAVDVSSGVGIAMKHSIGRGDAMKMLNA 392
 QY 276 FRKMFYK 284

Db 393 LRKKEVKK 401

RESULT 5

T21598

hypothetical protein F31D4.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21598

R:Mortimore, B.

submitted to the EMBL Data Library, March 1997

A:Reference number: 219447

A:Accession: T21598

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-443 <WILL>

A:Cross-references: EMBL:292832; PIDN:CAB07375.1; GSPDB:GN00023; CESP:F31D4.7

A:Experimental source: clone F31D4

A:Genetics:

A:Gene: CESP:F31D4.7

A:Map position: 5

A:introns: 13/3; 90/2; 149/1; 222/3; 290/3

Query Match 16.8%; Score 294.5; DB 2; Length 443;

Best Local Similarity 26.3%; Pred. No. 3.3e-18;

Matches 94; Conservative 63; Mismatches 124; Indels 77; Gaps 12;

OY 26 LVLGYLIVFGAVVSSVELPYEDLLRQELRKRRFLKEHCLSEQOLEOFLGRVLEA 85

DB 17 LIIIVFLIVCISGGLVFWLIEEPYQ---SELNDAMQHKIENNN---TARDAMMKKIFNN 69

OY 86 SNYGVSVLSNAGS-----NW-----NWDTSALFFASTVLSITGGY 121

DB 70 SLYLYIKNTSQRLLTFPIELSGYENOLGVGWSOOKMDW:WNVVLFFAGTICTTIGYG 129

OY 122 HTVPLSDGKACIIYSVIGIPETLLFLAVVQRITVH-----TRRPVLYFHIRMGFS 175

DB 130 HLYPMTDARMLTMTFALGILMLLVLDLDFGLTLITTKFPFQTKR--LMRRIMRCT 187

OY 176 KQVVALVNAV-----LLGFVVSCEFPIPAVSVLEDDMNFLESEYFCF 220

DB 188 KQPIEMKRIEQRHDLDFPLPLPVGIALIVTWIFICFVLSVMDHNTLLESFYFF 247

OY 221 ISLSTIGLGDYVGEISYONKRELYKIGTTC--YLLGLIAMLVLETCELHELKFRK 278

DB 248 TSLSTVGLDGLVPSSP-----RLITMFGFIIYGLISVSMVNL-----LQAKMK 292

OY 279 MEYVKKDKEDQVHILEHDQLSFSITDQAGMKEDOK---QNEPVTATOSSACVDS 332

DB 293 STYEAGRNDEKTPH--HOTLPTSLGLVLCFSPDEKKTIDYSERSLSRSTOTSLSPG 348

RESULT 6

T19860

hypothetical protein C40C9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T19860

R:Hembry, C.

submitted to the EMBL Data Library, March 1996

A:Reference number: 219188

A:Accession: T19860

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-334 <WILL>

A:Cross-references: EMBL:270266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1

A:Experimental source: clone C40C9

A:Genetics:

A:Gene: CESP:C40C9.1

A:Map position: X

A:introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match 16.8%; Score 294; DB 2; Length 334;

Best Local Similarity 29.2%; Pred. No. 2.6e-18;

Matches 71; Conservative 56; Mismatches 88; Indels 28; Gaps 11;

OY 26 LVLGYLIVFGAVVSSVELPYEDLLRQELRKRRFLKEHCLSEQOLEOFLGRVLEA 85

DB 14 LIIITFTYLLFGAVFDKLESEKDIWDEITERIDRLKHKN-FSEBDLHIF-----EA 67

OY 86 SNYGVSVLSNAGS-----NW-----NWDTSALFFASTVLSITGGY 145

DB 68 --IAKSIPOQAG--YQWQFAGAFYFAVITTVYGSHGAPSTNAGKLCMFALGVPMG 124

OY 146 LLEFLAVVQRITVYTR-----RPVLYFHIRMGFS-KQVVALVNAV-----LGFVTVSCF 195

DB 125 LIMQSIGERYNTEFVSLHKEFDSLH--OQGFYCLQDEVTPTHLVMSLTIGFVAVISG 181

OY 196 FFIPAAVSVLEDDMNFLESEYFCFISLSTIGLGDYVGEQYQ-KFRELKIGITCYL 254

DB 182 TY-----MFHTIE-KWSITDAIYFCMTITSTIGFGDLVPLQOVNALDDPPLYVAFATIMFIL 236

OY 255 LGL 257

DB 237 IGL 239

RESULT 7

T43361

probable potassium channel chain n2P20 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000

C:Accession: T43361

R:Wang, Z.W.; Salkoff, L.

submitted to the EMBL Data Library, August 1998

A:Description: Potassium channels in C. elegans.

A:Reference number: 222450

A:Accession: T43361

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-364 <MAN>

A:Cross-references: EMBL:AF083646; PIDN:AAC32857.1

Query Match 16.8%; Score 294; DB 2; Length 364;

Best Local Similarity 29.2%; Pred. No. 2.9e-18;

Matches 71; Conservative 56; Mismatches 88; Indels 28; Gaps 11;

OY 26 LVLGYLIVFGAVVSSVELPYEDLLRQELRKRRFLKEHCLSEQOLEOFLGRVLEA 85

DB 14 LIIITFTYLLFGAVFDKLESEKDIWDEITERIDRLKHKN-FSEBDLHIF-----EA 67

OY 86 SNYGVSVLSNAGS-----NW-----NWDTSALFFASTVLSITGGY 145

DB 68 --IAKSIPOQAG--YQWQFAGAFYFAVITTVYGSHGAPSTNAGKLCMFALGVPMG 124

OY 146 LLEFLAVVQRITVYTR-----RPVLYFHIRMGFS-KQVVALVNAV-----LGFVTVSCF 195

DB 125 LIMQSIGERYNTEFVSLHKEFDSLH--OQGFYCLQDEVTPTHLVMSLTIGFVAVISG 181

OY 196 FFIPAAVSVLEDDMNFLESEYFCFISLSTIGLGDYVGEQYQ-KFRELKIGITCYL 254

DB 182 TY-----MFHTIE-KWSITDAIYFCMTITSTIGFGDLVPLQOVNALDDPPLYVAFATIMFIL 236

OY 255 LGL 257

DB 237 IGL 239

RESULT 8

T43509

probable potassium channel chain n2P38 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000

C:Accession: T43509
 R:Wang, Z.W.; Salikoff, L.
 submitted to the EMBL Data Library, August 1998
 A:Description: Potassium channels in *C. elegans*.
 A:Reference number: Z22450
 A:Accession: T43509
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-329 <WAN>
 A:Cross-references: EMBL:AF083652; PIDN:AAC32863.1

Query Match
 Best Local Similarity 16.6%; Score 291; DB 2; Length 329;
 C:Species: *Drosophila melanogaster*
 Matches 80; Conservative 59; Mismatches 106; Indels 30; Gaps 10;

26 LVIGLTVLVGAVVSSVELPYEDLRQELKRLKEHEHCISEQLEQFLGRVLEA 85
 11 LIVCTLTLYLVGAADFALETENELQRLKLVORREKLTXTN-MSNDYE-----ILEA 64
 86 SNVGVSVLSNAGNNMDFTSALFPASTVLTSTGYGHTVPLSDGKACITVIGIPFT 145
 65 TI--VKSVPNHAG-YQWKEGSAFYFATVITTTIGYSTPTMDAGKVCMLYALAGIPLG 121
 146 LLEFVAVQRTVHVTRRPVLYFHIRMGSFQVAVIHAVLIGFVT--VSCFFPIPAVF 203
 122 LIMFOSIGERNMTFAK---LRFIRRAAGKOPT-VTSSDLIFCTGWMGLIFGAFMF 177
 204 SVLEDDNMFLESFYFCFISLTIGLGDYVPEGYNQKRELYKIGTIC---YLLGLIA 259
 178 SSVY-NMTYFPAVYVCFTVLTITIGFDYV-----ALQKRGSLQTOPETVFSVLR 226
 260 MLVVFELFCELHEKFRKMFYVKKDKEDQVHI 294
 227 ILFGLTVISAAMNLVLRFLMTNTERDERDEQEI 261

RESULT 9
 T32347
 outward rectifier potassium channel homolog twk-23 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32347
 R:Muray, J.; Mohlmann, P.; O'Neal, D.
 submitted to the EMBL Data Library, September 1997
 A:Description: The sequence of *C. elegans* cosmid F34D6.
 A:Reference number: Z21153
 A:Accession: T32347
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-336 <NUP>
 A:Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:F34D6.3
 A:Experimental source: strain Bristol N2; clone F34D6
 A:Gene: twk-23; CESP:F34D6.3
 A:Map position: 2
 A:Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3

Query Match
 Best Local Similarity 16.2%; Score 284.5; DB 2; Length 336;
 C:Species: *Caenorhabditis elegans*
 Matches 85; Conservative 54; Mismatches 107; Indels 35; Gaps 11;
 26 LVIGLTVLVGAVVSSVELPYEDLRQELKRLKEHEHCISEQLEQFL 79
 11 LIVCTLTLYLVGAADFALETENELQRLKLVORREKLTXTN-MSNDYE-----ILEA 67
 80 GRVLEASNYGVSVLSNAGNNMDFTSALFPASTVLTSTGYGHTVPLSDGKACITVIGIPFT 139
 68 --ILEAVI--VKSVPNHAG-YQWKEGSAFYFATVITTTIGYSTPTMDAGKVCMLYAL 122
 140 IGIPFTLLEFVAVQRTVHVTRRPVLYFHIRMGSFQVAVIHAVLIGFVT--VSCFFPI 197

DB 123 ACIPILIMFOSIGERNMTFAK---LRFIRRAAGKOPT-VTSSDLIFCTGWMGLIF 178
 QY 198 IPAASFVLEDDNMFLESFYFCFISLTIGLGDYVPEEGYNQKRELYKIGTIC---YL 253
 DB 179 GGAFMFSSYE-NMTYFPAVYVCFTVLTITIGFDYV-----ALQKRGSLQTOPETV 227
 QY 254 LGLIAMLVLETCEHEKFRKMFYVKKDKEDQVHI 294
 DB 228 FFLVFLIFGLTVISAAMNLVLRFLMTNTERDERDEQEI 268

RESULT 10
 T13807
 potassium channel protein - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
 C:Accession: T13807
 R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
 Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
 A:Title: ORK1, a potassium-selective leak channel with two pore domains cloned from *D. melanogaster*
 A:Reference number: Z17770; MUID:97075152
 A:Accession: T13807
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1001 <GOL>
 A:Cross-references: EMBL:U55321; NID:g3808067; PID:g3808068; PIDN:AAC69250.1
 A:Gene: ORK1
 A:Map position: 1

Query Match
 Best Local Similarity 15.1%; Score 264.5; DB 2; Length 1001;
 C:Species: *Caenorhabditis elegans*
 Matches 77; Conservative 51; Mismatches 106; Indels 29; Gaps 9;
 26 LVIGLTVLVGAVVSSVELPYEDLRQELKRLKEHEHCISEQLEQFLGRVLEA 85
 11 LIVCTLTLYLVGAADFALETENELQRLKLVORREKLTXTN-MSNDYE-----ILEA 64
 86 SNVGVSVLSNAGNNMDFTSALFPASTVLTSTGYGHTVPLSDGKACITVIGIPFT 145
 65 TI--VKSVPNHAG-YQWKEGSAFYFATVITTTIGYSTPTMDAGKVCMLYALAGIPLG 121
 146 LLEFVAVQRTVHVTRRPVLYFHIRMGSFQVAVIHAVLIGFVT--VSCFFPIPAVF 203
 122 LIMFOSIGERNMTFAK---LRFIRRAAGKOPT-VTSSDLIFCTGWMGLIFGAFMF 177
 204 SVLEDDNMFLESFYFCFISLTIGLGDYVPEGYNQKRELYKIGTIC---YLLGLIA 259
 178 SSVY-NMTYFPAVYVCFTVLTITIGFDYV-----ALQKRGSLQTOPETVFSVLR 226
 260 MLVVFELFCELHEKFRKMFYVKKDKEDQVHI 294
 227 ILFGLTVISAAMNLVLRFLMTNTERDERDEQEI 261

RESULT 11
 T27725
 hypothetical protein ZK1251.8 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T27725
 R:McMurray, A.
 submitted to the EMBL Data Library, December 1995
 A:Reference number: Z20411
 A:Accession: T27725
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-475 <MIL>
 A:Cross-references: EMBL:Z68222; PIDN:CAA92504.1; GSPDB:GN00022; CESP:ZK1251.8
 A:Experimental source: clone ZK1251
 A:Gene: CESP:ZK1251.8

| | | | | |
|-----------------------|------------------|--------------------|-------------|-------------|
| Query Match | 14.0%; | Score 245; | DB 2; | Length 631. |
| Best Local Similarity | 26.0%; | Pred. No. 1.1e-13; | | |
| Matches 99; | Conservative 52; | Mismatches 130; | Indels 100; | Gaps 16 |

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0Y 18 RSAMCEGF-----LVIGLYLIVEGAVNVSSE-----PRYEDILROELRK 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 200 KSMYMAFHHRKIOIGFHRFSVLIIVLYLLGAVMFWMEVRESREKAKTLDHVNNEHLDR 255
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 59 LKRFLDE---HECSGOOLEOFLGRV-----LEASNYSVLS--NASGNMWDETTA 107
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 260 LAENITDESNNNTITTEEMKVIYREMYIELMKIEGOYKSTYKLEADNNMKWTEPSA 31.9
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 108 LEFASVIVSTIGYHTVPLSDGKAFCIISYVIGIPELFLFLVAVQRIYVHTRRVLY 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 320 FEFSNNVYTTGYSIAPESITGLVAVGYEFIVPVLVLRDLOGFELVHLTK---LY 376
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 168 FHRMGFSK-----QVAVIAVHALGFTVSCFFIFPAAVSVLE 207
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 377 AH---GIQFRELNGKNKHVDEDEIISPIRKACILLASYLACTIIFYE----- 423
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 208 DDMWFLF-----SPYFCFISLSTIGADYVGR--GYMKFRELYK-----ITC 251
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 DELSGPEHGTOMDFLCYFSPISLSTIGADINPNNAVGNRRNRYENKIFADPISI 483
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 252 YLLGL-IAMLVLETCCEJHCLKRFKMYKKDKEDQVHIIHQSLFSISITQOAG 310
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 484 IFEGMAVTKVANNFTIYAV-ENGIFCAFLVENKLD-----ALVTRSSAS 528
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
0Y 311 MKEDOKONEPFAVROSSACVD 331
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 529 VKPDRRSTPKV--ORALSD 547
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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933
 15
 C:Species: *Caenorhabditis elegans*
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
 C:Accession: T28933
 R:Nelson, J.
 submitted to the EMBL Data Library, July 1996
 A:Description: The sequence of C. elegans cosmid C52B9.
 A:Reference number: 220545
 A:Accession: T28933
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-513 <NEL>
 A:Cross-references: EMBL:U064598; PIDN:AMC47976.1; GSPDB:GN00028; CESP:C52B9.6
 A:Experimental source: strain Bristol NZ; clone C52B9
 C:Genetics:
 A:Gene: CESP:C52B9.6
 A:Map position: X
 A:Insertions: 12/3; 54/3; 90/3; 158/1; 173/1; 227/3; 299/3; 346/2; 378/2; 405/1; 452/3

| | | | | |
|-----------------------|--------|--------------------|-------|-------------|
| Query Match | 13.9%; | Score 244; | DB 2; | Length 513, |
| Best Local Similarity | 22.8%; | Pred. No. 1.1e-13; | | |

| | Matches | 81; | Conservative | 64; | Mismatches | 95; | Indels | 116; | Gaps | 15 |
|----|---------|---|--------------|-----|------------|-----|--------|------|------|----|
| QY | 26 | LVIGLYLYVFGAVVTSVVELPYEDLLRQLRKIKRRFLFEHBCLSQOOLEQFLGVLEA | 85 | 11: | 11: | 11: | 11: | 11: | 11: | |
| Db | 65 | LVTLLEFLYLITAGAFLEFRYLEAPKE--LEDSDNNISR--EAFRAINQELFEQVLKMFQA | 119 | 11: | 11: | 11: | 11: | 11: | 11: | |
| QY | 86 | -SNVGSV--LSNASGMWN--WDFIALPFASTVLT-----TGXYHTVP | 125 | 11: | 11: | 11: | 11: | 11: | 11: | |
| Db | 120 | YRNQFLITAKHLNKTEDEVELMTFEPMSMFPAATVITTIQVKNRSQNRVFSRGYNLVP | 179 | 11: | 11: | 11: | 11: | 11: | 11: | |
| QY | 126 | LSDGCAFLCITLYSVIGIPETLLFLAVAVRIIVHVTBRPVLEFHLRWGSKVY----- | 178 | 11: | 11: | 11: | 11: | 11: | 11: | |
| Db | 180 | IIVTGKAVACIIIFALIGIPLLVTIADIGKFLSEPLS--YLTKSYR--GPKRRLRQSKRI | 235 | 11: | 11: | 11: | 11: | 11: | 11: | |
| QY | 179 | -----VAIVHAVYLGFVTVSC | 194 | 11: | 11: | 11: | 11: | 11: | 11: | |
| Db | 236 | TSQYNSQSSQSRSSVWGSSKAGSMNIHIDSDSEDSAGDELRIPYFMVILVILAVTALIG | 295 | 11: | 11: | 11: | 11: | 11: | 11: | |
| QY | 195 | FFFTPAAVFSVLEDDM--NFLSESYFCFISLTGIGDGYVPGEGYKNCKFELYKIGITC | 251 | 11: | 11: | 11: | 11: | 11: | 11: | |
| Db | 296 | FLF-----QSMWHELFYEAFLYFCFTIMAYVGEDIVPNE-----QVVVFVTMA | 338 | 11: | 11: | 11: | 11: | 11: | 11: | |
| QY | 252 | YLLGLGLIMLVLELFC-ELHEHLKFRMRMYVKDKDEDQ-----WHITEN | 296 | 11: | 11: | 11: | 11: | 11: | 11: | |
| Db | 339 | YIIFGL-----SLATMCIIDLAGTEYIRKIRIHILGTCKMEDAKGAVVTGIGQAGENHLHK | 389 | 11: | 11: | 11: | 11: | 11: | 11: | |

Search completed: February 14, 2001, 12:56:12
Job time: 37094 sec

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